

FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGCTGCTAGGCCTC
TGTGCCCGGGCTTGGAAATTGCGTGC~~GG~~GATGGCAGCTCCGGATGACCCGCCGGACC~~G~~C
CGCAAATAAGGTGGCCCTGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATGCCCGC
GTTTGGCCAGGACGGGCCATGTGGT~~CGT~~CAGCAGCGGAAGCAGCAGAATGTGGACCAG
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGCACCGTGTGCCATGTGGGAA
GGCGGAGGACCGGGAGCGGCTGGTGGCACGGCTGTGAAGCTCATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTGTAACCTTCTTGGAAAGCATAATGGATGTCACTGAGGAGGTG
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCAAGCCTGATGACAAAGGAGTGGTGC
AGAAAATGGAGAAACGAGGAGGCGCTCAGTGGT~~GAT~~CGTCTTCCATAGCAGCCTCAGTC
CATCTCTGGCTTCAGTCCTTACAATGT~~CAG~~TAAAACAGCCTGCTGGGCTGACCAAGACC
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGA~~ACT~~GCC~~T~~AGCACCTGGACTTCAA
GA~~C~~TAGCTTCAGCAGGATGCTGGATGGACAAGGAAAAAGAGGAAGCATGAAAGAACCC
TGC~~G~~GATAAGAAGGTTAGGCAGGCCAGAGGATTGTGCTGGCATCGTGTCTTCTGTGCT
GAAGATGCCAGCTACATCACTGGGAAACAGTGGTGGTGGAGGAACCCGTC~~CC~~GCCT
CTGAGGACCGGGAGACAGCCCACAGGCCAGAGTTGGCTTAGCTCCTGGTGTCTGC
ATTCA~~CC~~ACTGGCTTCC~~CC~~ACCTCTGCTCACCTACTGTTCACCTCATCAAATCAGTTCT
GCCCTGTGAAAGATCCAGCCTCCCTGCCGTCAAGGTGGTCTTACTCGGATTCTGCT
GTTGTTGTGGCTTGGTAAAGGCCCTCCCTGAGAACACAGGAACAGGCC~~T~~GCTGACAAGGCT
GAGTCTACCTGGAAAGACCAAGATA~~TTT~~TCCTGGCCACTGGTGA~~AT~~CTGAGGGTGA
TGGGAGAGAAGGAACCTGGAGTGGAGGAGCAGAGTTGCAAA~~TT~~ACAGCTTGCAATGAGG
TGCAAATAAAATGCAGATGATTGCGCGGCTTGAAAAA

FIGURE 2

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672
><subunit 1 of 1, 278 aa, 1 stop
><MW: 29537, pI: 8.97, NX(S/T): 1
MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVVS
SRKQQNVQAVATLQGEGLSVTGTCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG
SIMDVTEEVWDKTLDINVKAPALMTKAVVPEMEKRGGSVVIVSSIAAFSPSPGFSPYNVSK
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRGEPEDC
AGIVSFLCSEDASYITGETVVVGGGTPSRL
```

Important features of the protein:

Signal peptide:

amino acids 1-15

N-glycosylation site.

amino acids 183-186

N-myristoylation sites.

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

Microbodies C-terminal targeting signal.

amino acids 276-278

FIGURE 3

GGCCCTGAGCTCGCCCTCGGGCCCAGATAGCGGCATCGAGAGCGCCTCCGTGAGGACCAGGGCG
CAGGGGCCGGCGGGCAAAGGAGGATGAGGGGGCGCAGCAGCTGTCGACCCCTGCAGAACCGAGTGGC
GCGGCTGGAGGAGGAAACCGAGACTTCTGGCTGCGCTGGAGGACGCATGGACAGTACAAACTGC
AGAGCACGGCTGCGTGAGCAGCAGGAGGAGATGTGGACTCGGGCTGCGGTTAGAGCTGTCGCG
CCAGGCTGGGGGGCCTGCGCTCCTGAATGGCTGCCCTCCGGTCTTTGTGCGCTGCACCTCATAC
AGCCCCCTGGGGGTGCCACGCCATGTGCTGGCATGGTGCCTGCCCTGCCCTGGAGATG
AAGTTGCGCTCTGACAGAGGGAGGAGCAGTGACAAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT
GAGGTGAACAGGCTGGGAAGGTGGCTTCAGCTGCTCAGAGGAGAAGAGGAGGAGGAGGCC
CAGGCGAACCTTAACCTCGCAGAAATAGGATCAGCAACTCAGTCAGAGGGCGGGCACCCAG
GGAGTCGCCAGAGGAAAGGGCCCAGAGCTTGCCTTGAGGAGTTGGATCGACCATTCAGGGTCC
AGAGCAGTGGTGGAGCAAGGCCAGTTCAGGCCGCCAGGTCCCCCTGCCACAGCCTCAGAGTG
GCGGCTGGCCCAAGGCCAGCAGAACAGATCCGGAGCTGGCTATCAACATGCCATGAAGGGAGGAGCTTA
TTGGCGACTGCTGGCCACAGGAAAGCAGCTCAGGCCCTGAACGCCAGCACAGCCAGCGTATCCG
GAGCTGGAGCAGGAGGCCAGAGCAGCTGGGGGCCAGAGCTGAGTAAGGGCCAGAGGAGCTGGGGAGCT
CGAGGGCAAGGAGCTCAGGATGCTGGCAGCGGCTCGGGCTCAGGAGTTCAGGAGGGCTCGCTG
CGGCCACAGCCAGGTGCAAGTGCAGGAGAACAGCAGCTACGGAGCGGCTGGTGTACTGTC
GCCAGAGTGAGAACGACTGCAAGAGCTCGAGCGAACAGTGCAGCTATGCCAGCAGCAGGACA
GCTGCAAGGGCGCTTCCGGAGAGCACCGAGCAGAACGGCCCTTGAGGAGCAGAACATGAGAACGGC
AGCACCGGCTCAAGGAGCTGGAGCTGAAGCATGAGAACAGCAGAACAGAACAGATCTGAAGATTAAAGCGAA
GAGATCGGCCCTTCAAGGAGAGGGCAGTGGCAGCAAGCTCTGTGGTCAACCTGGAAACAGCA
GCAGAACAGATTGAGGAGCAGAACAGTGGCTGGACAGGAGATGGAGAACGGTGCTACAGCAGCGGG
CGCTGGAGGAGCTGGGGAGGAGCTCCAAGCGGGAGGCCATCTGGCCAAGAACAGGAGGCCCTGATG
CAGGAGAACAGCGGGCTGGAGGCAAGGCCAGATGCCAGCCGCCCTAACAGGAGAACATCGTGG
AGTGTCCAGCGGGCTGGAGCACCTGGAGAACGGAGCTTCCGAGAACAGGGGCCATCGGGAGGGCA
GCGCCAGAGGCCAGCAGATCCGGGGAGGAGCTGAGGAGCAGGCCCTAACAGGAGAACATCGTGG
AAGCAGGCCCTGGAGATCGACGCCAGCTGAGGAGCGGGAGTCTGCTGTCCCCAGGAGGAGCCGAC
GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAATGAGGCCATCA
CATGCCGCCAGCGGGCTTCCGGGCCATCAGGCCCTGGAGAACAGGAGAACATCGTGG
AAGCTCACTCTCATCTCATCTCAGAACAGGCCAGAGGGCTCTCTGCAAGTATTTGACAAGGTGGTGAC
GCTCGAGAGGAGCAGCACCGAGCACGAGATTGCTCTGGAACTGGAGATGCAAGTGGAGGAGCAGC
AGAGGCTGTGACTCGCTGGAGTGGCCCTGGAGGGCAGGCCCTGGAGATGGACGCCAGCTGACC
CTGCAGCAGAACAGGAGCACGAGCAGAACATGCAGCTCTGCAAGCAGAGTCAGAACCCACTCGGTGA
AGGGTTAGCAGACAGCAGCAGGAGGACTATGAGGCCGGATTCAACCTCTGGAGAACAGGAGTGGGGCGTT
ACATGTGGATAAACCGAACATGAAACAGAACAGCTCGGGCTGTAACGCTGTAGGCCACAGCAGGGGT
GGGGAGAACAGGGAGCTGCTGGAGGGCAGAACAGGCTCTGGAAATGAAGATGAGCTCCACCTGGC
ACCCGAGCTCTCTGCTGTCCCCCTCACTGAGGGGGCCCCCGAACCGGGAGGAGACGCCGACT
TGGTCCACGCTCCGGTACCCCTGACCTGGAAACGCTCGAGCCCTGTGTTGGTGGAGGAGCAGGGGCCCC
GAGGA^{ACT}GAGGCAGCGGGAGGCGCTGAGGCCCTGGGGGGGGTCTGTGGTGAGGCC
CTGCCCTGGAACTTTGGGCCCTTGTCCAAGGCCCGGGAACTGCGACAGGCCAGCCGGGATGA
TTGATGTCCGAAAAAACCCCTGTAAGCCCTCGGGCAGACCCCTGCCCTTGGAGGGAGACTCCGAGCCT
GCTGAAAGGGCAGCTGCTGTGTTGCTGTGAAGGGCAGTCTTACCGCACACCTTAAATCCAGG
CCCTCATCTGTAACCTCACTGGGATCAACAAATTGGGCCATGGCCAAAAGAACACTGGACCCCTCATTT
AACAAAATAATATGCAAATTCCACCCTACTTCCATGAAGCTGTGGTACCCATTGCGCCTGTG
TCTTGCTGAATCTCAGGACAATTCTGGTTTCAGGGCTAAATGGATGTGTTGAGTTCAAGGGTTTG
GCCAAGAAATCATCACGAAAGGGTCGGTGGCAACCAGGTTGTGGTTAAATGGCTTATGTATATAGGG
GAAACTGGAGACTTTAGGATCTTAAAAAACCATTAAATAAAAAAATCTTGAAGGGAC

FIGURE 4

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465
<subunit 1 of 1, 830 aa, 1 stop
<MW: 95029, pI: 8.26, NX(S/T): 2
MEQYKLQSDRLREQQEEMVELRLRLELVPGWGLLLNGLPPGSFVPRPHTAPLGGAHAV
LGMVPPACLPGDEVGSEQVRGEQVTNGREAGAEILTEVNRLGGSSAASEEEEEEEPPRRTL
HLRRNRISNCQRAGARPGSLPERKGPELCLEELDAAIPGSRAVGGSKARVQARQVPPATAS
EWRLAQAAQQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRLEEQAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQLKEKKQATERLVSLSAQSEKRLQE
LERNVQLMRQQQGQLQRRRLREETEQKRRLEAEMSQRQHRVKEELKHEQQQKILKIKTEEIA
AFQRKRRSGSNGSVSLEQQQKIEEQKKWLDQEMEKVLQQRRALEELGEELHKREAILAKKE
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAQSQQQIRGEIDS
LRQEKDSSLKQRLEIDGKLQRGSLLSPEEERTLFQLDEAIEALDAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMALKSYLSSETRALLCKYFDKVVTLREEQHQQQIAFSELEMQLEEQQR
LVYWLVALERQRLEMDRQLTLQQKEHEQNMQILLQQSRDHHLGEGLADSRQYEARIQALEK
ELGRYMWIINQELKQKLGGVNAVGHSGGEKRSLCSEGGRQAPGNEDELHLLAPELLWLSPLTEG
APRTTRETRDLVHAPLPLTWKRSSLGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG
PLSKPRRELRRASPGMIDVRKNPL
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Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

FIGURE 5

ATTCTCCTAGAGCATCTTGGAAAGCATGAGGCCACGATGCTGCATCTGGCTTTGTCTGCT
GGATAACAGTCTCCTCCAGTGTCAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA
CTGTGGCTGTGCCAGCGACACCCAGGTGTGGAAACAAGATCTACAACCCCTCAGAGCAGTG
CTGTTATGATGATGCCATCTTAAAGGAGACCCGCCGTGTGGCTCCACCTGCACCT
TCTGGCCCTGCTTGAGCTCTGCTGCCCAGTCTTTGGCCCCCAGCAGAAGTTCTTG
AAGTTGAGGTTCTGGGTATGAAGTCTCAGTGTCACTTATCTCCCATCTCCGGAGCTGTAC
CAGGAACAGGAGGCACGTCTGTACCCAAAAACCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACCTCGGAGAGAAC
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTGAGAGGGAGGCCAGCTGGGATGGC
CAGACTTCAGGGGAAGAATGCTTCCGTTCAGCTCCCTCCAGCTCCCTCCGCTGAG
AGCCACTTCATCGGCAATAAAATCCCCACATTACCATCT

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700
><subunit 1 of 1, 125 aa, 1 stop
><MW: 14198, pI: 9.01, NX(S/T) : 1
MRPRCCILALVCWITVFLLQCSKGTTDAPVGSGLWLQPTPRCGNKIYNPSEQCCYDDAILS
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRLGMKSQCHLSPISRCTRNRHVLYP
```

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

FIGURE 7

CCACCGCGTCCGCCACCGCTCCGGGTGCCACTCGCGGCCGGCCGCGCTCCGGCTTCTCT
TTTCCCTCCGACGCGCACGGCTGCCAGACATTCCGGCTGCCGGTCTGGAGAGCTCCCCG
AACCCCTCCGGAGAGGGAGCGAGGCCAGGGTGGCCCCGGGCTGGCTCG
GAGAAGCGGGGACGAGCGAGGATGAGCGACTGAGGGCAGCGGGCACTGACCGAGTT
GGGGCGCGACTACCGGAGCTGACAGCGCATGAGCGACTCCCCAGAGACGCCCTAGCCCG
GTGTGCGCGCCAGGGAGCGAGGTGGGCTGGCTGTAGTGGTCCGCCCCACGCCGG
TCGCCGCCGGCCCAGGATGGCGCTGGCAACCCGGGCCGCGCCCGCTGCTACCCCTG
CGCCCGCTGCGAGCCGGCTCCGGCCGCGCCCTGCGCTCATGGACGCCGGCTCCGGCTG
GCCGCAGGGACGTGGTAGGGATGCCAGCTTCACTGCGATGGCAGTTGGCGCCTCCA
GTTCCCTCTGGTCACCTGCTGCCTGATGGTGGCTCTGTGCACTGGAGATCCGCTGGAG
AAGCTGGCCCAAGGACCCAGAGCAGCCGGCCAGGAAGCGTGAGCACGCCACTGGGACGG
CCCGGGCGGGTAACGACTCGGGCCCGCGAGGGACGAGGGCGCAGGGCCGGACT
GGAAGAGCAAGAGCGCCGTGGCTCGCCGGCGTGGAGCAAGCTGAAGCAGGCC
TGGGTCTCCCAGGGCGGGGGCGCAAGGCCGGGATCTGCAGGTCCGCCCGGGGACAC
CCCGCAGGCCAGCCCTGGCCGAGCCGCCAGGACGCGATTGGCCCGAAGCTGCCCA
CGCCCGAGCCACCCGAGGAGTACGTGTACCCGACTACCCTGGCAAGGGCTGCGTGGACGAG
AGCGGCTTCGTACCGATCGGGAGAAGTTCGCGCCGGCCCTCGGCTGCCGTGCCT
GTGCACCGAGGAGGGCCGCTGCGCGAGCCCGAGTGCAGGGCTGCACCCGCGCTGCA
TCCACGTCGACACGAGCCAGTGCTGCCCGCAGTGCAAGGAGAGGAAGAAACTACTGCGAGTT
CGGGCAAGACCTATCAGACTTGGAGGAGTTCGTGCTCTCCATGCGAGAGGTGCGCTG
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTCAGCGTGTCCCAGACGGAGTGTGGACC
CTGTGTACGAGCCTGATCAGTGCTGCTCCATCTGAAAAATGGTCAAAGTGCCTTGAGAA
ACCGCGGTATCCCTGCTGGAGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTAC
TTATGAGGAAGGCACATGGAGAATCGAGCGCAGGCCATGTCACGAGACATGAATGCAGGC
AAATGTACGCTCCAGAACACAAACTCTGACTTTCTAGAACATTTACTGATGTGAA
CATTCTAGATGACTCTGGAACTATCAGTCAAAGAACACTTGTAGAACATTTACTGATGTGAA
TTGTTGGTACTTTCTTCTGATAACAGTTACTACAACAGAACAGGAATGGATATTT
AAAACATCAACAAGAACACTTGGGATAAAATCCTCTCTAAATAAAATGTGCTATTTCACAG
TAAGTACACAAAAGTACACTATTATATCAAATGTATTTCTATAATCCCTCATTAGAGAG
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AAAAAAAAAAAAAAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818
><subunit 1 of 1, 325 aa, 1 stop
><MW: 35296, pI: 5.37, NX(S/T): 0
MPSSTAMAVGALSSLLVTCLMVALCSPSIPLEKLAQAPEQPGQEKRHATRDGPGRVNEL
GRPARDEGGSGRDWKSKGRLLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTPQAELA
AAAQDAIGPELAPTPPEPPEEYVYPDYRGKGCVDESGFVYAIKEKFAPGPSACPCLCTEEGPL
CAQPECPCRLLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCEANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEEGTWR
IERQAMCTRHECRQM

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

FIGURE 9

CAGCCACAGACGGGT**ATGAGCGCGGTATTACTGCTGGCCCTCCTGGGTTCATCCTCCCAC**
TGCCAGGAGTGCAGGCCTGCTCTGCCAGTTGGACAGTTCAGCATGTGTGGAAGGGTGTCC
GACCTACCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGTTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCAAGTGA
GAGCCTGGTCTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCCGCGTC
ACTGAGCACCGGATGGGCCCGGCTCTCCCTGATC
TCCTACACCTTCGTC
GCCCCCAGAGACCCAGGATCTTGAGGTGCCAGTCTGCTTGTCTATGG
TTGGGCCACAGCCCCCAGCAGACCCAGGATCTTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGACAACAGAAAGAGATCTGCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGAGGAGGCATCTTCTCAATCTGAGAGTCCAGGGATGCATGCC
CCAGGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCGTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTCTGACCTGTC
CATGGGGACCACCAATTGACACACGGAAAC
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGCAGGT
GTGTCAGGAGACGCTGCTGCTCATAGATGAGGACTCACATCAACCTGGTGGGACAAAAG
GCTGCAGCACTGTTGGGCTCAAATTCCAGAACGACCACCATCCACTCAGGCCCTCTGGG
GTGCTTGTGGCTCTATAACCCACTTCTGCTCTCGGACCTGTC
AATAGTGCCAGCAGCAG
CAGCGTTCTGCTGA
ACTCCCTCCCTCCTCAAGTGCCCTGTCCAGGAGACGGCAGTG
CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCA
GGCGCCACTCATTGTTATGATGGGTACATTCA
CTCTCAGGAGGTGGCTGTCCACCAAAAT
GAGCATTCA
GGGCTGAGGGCTGGAGTCTCTCACTTGGGGGTGGGCTGG
ACTGGCCCCAGCGCTGTG
GTGGGGAGTGGTTGGCTCTGCT**TAAC**TCTATTACCCACGATTCTC
ACCGCTGTG
CCACCCACACTCAACCTCCCTGACCTC
ATAACCTAATGGCTTG
GACACCAGAGTCTTCC
CCATTCTGTC
CATGAATCATCTTCCCCACACACA
ATCATTCA
TATCTACTCACCTAACAGCA
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CCTATGGGAGAGGGACGCTGGAGGAGTG
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ATACAGACCC
CTGTC
CTTCA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847
><subunit 1 of 1, 437 aa, 1 stop
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ESGPQVSVLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEICPKGTTHYDGLLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGGTTIMTHGNLAQEPTDWTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGKCGSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAVPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

FIGURE 11

CGACG**ATG**CTACGCGGCCGGCTGCCCTCTCCGGACCTCCGTAGCGCCTGCCGCCGCTG
GCTGCGGCCGCTGCTCTCGTCGCTTGCGCCTGCTCTTCTAGAGCCGAGGGACCCGGTGGC
CTCGTCGCTCAGCCCCATTTCGGCACCAAGACTCGTACGAGGATGTCAACCCCGTGCAT
TGTGGGCCCGAGGCTCCGTCGCGGGACCTGAGCTGCTGGAGGGGACCTGACCCCGGTG
CAGCTGGTCGCCCTCATTCGCCACGGCACCCCGTACCCCGTCAAACAGATCCGCAAGCT
GAGGCAGCTGCACGGGTTGCTGCAGGGCCGGTCCAGGGATGGCGGGCTAGTAGTACCG
GCAGCGCGACCTGGGTGCAGCGCTGGCGACTGGCCTTGTGTACGCGGACTGGATGGAC
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCTCGCT
CTTCCCCGCCCTTTCAAGCCGTGAGAACTACGGCCGCTGGCGTCATCACCAAGTTCCAAGC
ACCGCTGCATGGATAGCAGCGCCCTTCTCGCAGGGCTGTGCAGCACTACCACCCCTGGC
TTGCCGCCGCGGACGTCGAGATAATGGAGTTGGACCTCCAACAGTTAATGATAAACTAAT
GAGATTTTTGATCACTGTGAGAAGTTTAACGAAGTAGAAAAAAATGCTACAGCTTT
ATCACGTGAAAGCCTCAAAACTGGACAGAAATGCAAGAACATTAAAAAGTTGAGCT
ACTTTGCAAGTGCAGTAAATGATTTAAATGAGATTTAAATTCAGTGGTGTGATGTTTTGACATAGATG
TTCATTGACCTGGCAATTAAAGGTTGAAATCTCCTGGTGTGATGTTTTGACATAGATG
ATGCAAAGGTTAGAATTTAAATGATCTGAAACAATATTGAAAAGAGGATATGGTAT
ACTATTAAACAGTCAGTCCAGCTGACCTTGTTCAGGATATCTTCAGCACTTGACAAAGC
AGTTGAAACAGAAACAAAGGCTCAGCCAATTCTCTCCAGTCATCTCAGTTGGTCATG
CAGAGACTCTTCTTCACTGCTTCTCATGGGCTACTCAAAGACAAGGAACCCCTAACAA
GCGTACAATTACAAAAACAAATGCACTGGAAAGTTCGAAGTGGTCTCATGACCTTATGC
CTCGAACCTGATATTGTGCTTACACTGTGAAAATGCAAGACTCCTAAAGAACATTCC
GAGTGCAAGATGTTATTAATGAAAGGTGTTACCTTGGCTACTCACAAGAAACTGTTCA
TTTTATGAAAGATCTGAAAGAACCTACAAGGACATCCTTCAGAGTTGTCAAACAGTGGAA
ATGTAATTAGCAAGGGCTAACAGTACATCTGATGAACAT**TGA**TAAGTGAAGAACATT
AATTCTTCTAGGAATCTGCAATGAGTGTATTACATGCTGTAAATAGGTAGGCAATTCTTGTATT
ACAGGAAGCTTATATTACTTGAGTATTCTGTCTTTCACAGAAAAACATTGGTTCTC
TCTGGGTTGGACATGAAATGTAAGAAAAGATTTCACTGGAGCAGCTCTTAAAGGAGAA
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TTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTCATATAAACACTTGAAAAGTGCT
GGAGTAACAAATATCTCAGTTGGACATCTTAACTTGATTGAACATGCTAGGAACCTTAC
AGATTGTTCTGCAGTCTCTCTTCTCAGGTAGGACAGCTAGCAATTCTTAAATC
AGGAATATTGTGGTAAGCTGGGAGTACACTCTGGAAGAAAGTAACATCTCCAGATGAGAAT
TTGAAACAAGAAACAGAGTGTGAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAA
TGAAAATAAATTTTGTATTATTATGAAATATTGAAACATTGTTCAATAATTCTT
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AAGTCAGATAGTTAGAATCGAAGTCTTCAATCCATTGCTTAGCTAACCTTTCTGTT
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TAAAGAAAATTCTTGTGACTTTAAAAAAAAA

FIGURE 12

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><subunit 1 of 1, 487 aa, 1 stop
><MW: 55051, pI: 8.14, NX(S/T): 2
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RDLGAALADWPLWYADWMDGQLVEKGRQDMRQIALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFLQGLWQHYHPGLPPPVDADMEFGPPTVNDKLMRRFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVAATLQVPVNLDLNADLIQVAFFTCSDLAIKGVKSPWCVDVFDIDDA
KVLEYLNNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSSLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLIFVLYHCENAKTPKEQFRV
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

FIGURE 13

GGGACTACAAGCCCGCCGCCGTGCCGCTGGCCCCCTCAGCAACCCCTCGACATGGCGCTGAGGCCGCCACCGCGAC
TCCGGCTCTGGCGCTGGCGTGCACTCTTCCTGCTGCTGCTGTTTCAGGGGCTGCCGTGATAGGGGCTGAAATACT
TCAAAATCCGAATCGAACCCCGTAGGATCAGGAAATTGAAAGTGTGGAACGTGCTTGATCATTAACGGATTCGC
AGACAAGTGGACCCCAAGGATCGAGTGGAAAGAAAATTCAAGATGAAACACCATATGTTTTTGACAACAAAA
TTCAGGGAGACTTGGGGGCTGTCAGAAAATCTGGGGAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTTCAGCCCTTATCGCTGTGAGGCTGTCAGGAATGACCCGAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCAGTGTGCAAGGCTGTAACAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGACTGAGGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCCACTGCCACGGATT
CCAGAGCCAATCCCAAGATTGCAATTCTCTTCCACTAAACTCTGAAACAGGCACTTGGTGTTCACTGTCG
TTCACAAGGAGGACTCTGGGCACTACTGATTGCTTCAATGACGCCAGGGCTCAGCCAGGTGAGGCCAGG
AGATGGAAGGACTTATGACCTGAACATTGGCGGAATTATTGGGGGGTTCTGGTTGCTCTGCTGACTGCCCTGA
TCACGTGGGATCTGCTGATCACAGACGTGCTGACTCTACAAATAACAGGATGGAGAAAGTACAAGA
ACCCAGGAAACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCAGTTCAGACACAAAGTCATGTTG
TGATCTGAGACCCGGCTGGCTGGAGACGCGCACAGAGCAGCCTGCACTACACCTCTGCTAGAAACTCTGTCAA
GGCACGGAGACTGATGCCATCGGACAGAGCTAGAACACTTCACTGAGAAGCTTTCGCTTGGCCAAGTGGACA
CTACTCTTCTACTAACAGGACACATGAATAGAAAGATTCTTCAGAAGCTTTCGCTTGGCCAAGTGGACA
GGAAGCGAAACTGGGTGCGTCACTGAGTTGGTCTCTAATCTGTTCTGGCTGATCTCCGATGAGTATTAGG
GTGATCTAAAGAGTTGCTCAGCTAAAGCCCGTGTGGCCCTGTGAGACCCAGTGTACCAACTGTCGTT
CAGCAGCCACGACGACCCATGTGAGATGGCGAGGTGGCTGGACAGCAGCAGCGCATCCGGCGGAAACCCA
GAAAAGGCTTCTAACAGCAGCCTACTTCACTGGGCCACAGACACCCAGCAGTTCTTAAAGGCTTCTG
TGATCGGTGTTGCACTGTCATTGAGCAGCTTGTGAGCTTGTGATCAGCATTGTTGAGGAAACAAAATCAGGAAG
GTAAAATGGTTGCTGGAAAGGGAGACTTCTGAGGAAACCTCTGCTGTCACAGGGTGTGAGGATTAAAGGAAA
ACCTTCGTTAGGCTAAAGTGTGAAATGGTACTGAAATATGTTCTATGGTCTGTTTATTTTAAATAATT
TACATCTAAAGTGTAAAGATGATTGATTATGAAAGAAAATTCTATTTAAACGTGAAATATAATTGT
CATACAATGTTAAATAACCTATTTTTAAAAAGTTCACITTAAGGTAGAAGTTCACAGTGTAAAT
TGAAAATATAAAATAATTAAAGATGATTGTTACCAAGGAACCTCTCATGGAGGTTACTGTGATGTTCTTCT
CACACAGGTTAGCCTTTCACAGGAAACTCATGTCATCTACACATGACCATAGTTGCTTAGGAAACCTT
TAAAATTCAGTTAACGCAATGTTGCAATCTGTTGATCTCTTCAAAAAGAACCTCTCAGGTTAGCTTGA
GCTCTCTCTGAGATGACTTAGGACAGTGTGACCCAGGGCACCCAGAACCCCTCAGATGTCATACACAGATG
CCAGTCAGCTCTGGGGCTGGCAGTGGCTGTCAGCTTACTGAGCTACTGTTGCTGCTGCTGAGGCC
GCCATCTTGGGCCCTGGCAGTGGCTGTCAGCTTACTGAGCTTACTGAGCTGGCCCTGGCTCATCCACAGC
TCTCAGGGGGCACTGCAAGGGACACTGGTGTCTTCAGTAGCGTCCCAGCTTGGCTCTGTAACAGACCTCT
TTTGGTTATGGATGGCTCACAAATAGGGCCCAAATGCTATTTTTTAAAGTTGTTAATTATTGGT
AAGATTGCTTAAGGCAAAGGCAATTGCGAAATCAAGTGTCAAGTCAATAACACATTAAAAGAAAATGGAT
CCCACTGTTCTCTTGCACAGAGAAACCCAGACGCCAGGGCTCTGCAATTCAAAACACATGAT
GGAGTGGGGCAGTCCAGCTTTAAAGAACGTCAGGGAGCAGCAGGTTGAAAGGCCGGGGAGGAAAG
TGAACGCCCTGAATCAAAGCAGTTTCAATTGACTTTAAATTTTCACTCCGGAGAACACTGTCCTCCATT
TGTGGGGGACATTAGCACATCACTCAGAAGGCTGTGTTCAAGAGCAGGTGTTCTAGCCTCACATGCCCT
GCCGTGGACTCAGGACTGAGTGTGCTAACAGGAGCTGCTGAGAAGGAGCACTCCACTGTTGCTG
GAATGGCTCTACTACTCACCTGTTCTTCAGCTCCAGTGTCTGGGTTTTTAACTTGTGACGCTTTTTT
AATTGCAATCATGAGACTGTGTTGACTTTTTAGTTATGTTGAAACACTTGGCCGAGGCCCTGGCAGAGGCA
GGAAATGCTCAGCAGTGGCTCAGTGTCTCTGGTCTGCTGCAATGGCACTCTGGGATGCTTACAGATGCAAGTTC
CTCCCATCATGGCCACCTTGGTAGAGAGGGATGGCTCCACCCCTCAGCGTTGGGATTACGCTCCACCTCT
TCTTGGTTGTCAGTGTGATAGGGTAGCCTTATTGCCCCCTCTCTTACACCTAAACCTCTACACTAGTGCA
TGGGAACCCAGGCTGAAAGAAGAGAGAAGTGAAGTGTGACTCAAGACTGAGGCGATACGAGGCTGTGATTCT
CGGAAAAGGAATACTCGTGTATTAAAGATGAAATGTGACTCAAGACTGAGGCGATACGAGGCTGTGATTCT
GCCTTGGATGGATGTGCTGATCACAGATGCTCACAGACTTGTACTAACACCCGTAATTGGATTGTTAAC
CTCATTATAAAAGCTCAAAAAACCCA

FIGURE 14

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLCARLPDFLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLK IWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIA NDGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

FIGURE 15

CAGGACCAGGTCTTCTACGCTGGAGCAGCGGGGAGACAGCCACCATGCACATCTCGTGGTCCATGCCATGGTG
ATCCATGCGACGGCCGGCCCTCGAGGCCAGCAGCAGGTTCCAGGCCGTGCTGGACATCTGGGTTCCGGAG
GAGAACGCCACTGCCACCCTTCCTGGGACACATCGGAGGCCGTGCTGCTTCCTGACTGGCTGAAGCTG
CGCATGATCGGTTTGAGGTGCTCCGGCTGGAGCAGCCGCCTGCAGGACTGGAGGCCAGCAGCTGCTGCTG
TCGAGTCGTTGGCATCCCCGTGTCAGCATGAGCAAACCTCTCCAGTTCTGGACCAGGCAGTGGCCAC
GACCCCGAACACTCGGAGCAGAACATCGGAGAAAGTACATGCCACCTGGAGGTCCAGCATGAGGCC
GGGCCCTCCGGAGGCCAGACTTCACTTCTGTCAGGCCCTCCGGCCGGAGACAGCACAGAGGCA
CCCCAAACAAAGAGCAGCCAGAGCAGCCCATAGGCCAGGGCGATTGGGTGGGACCCAGCTCCGGTGTG
GGCCCTGAGGACGACCTGGCTGGCATGTTCTCCAGATTTCGGCTCACGCCGACCCCTGGTGAGAGCTCC
AGTGGCCGGCCCGTGGCCCTCGAGCAGGCCCTGGCCAGAGCTGGCCGGCTGCTCCAGGGCAGGCC
GAGGTGGCCGGCATACGGCTGCGTCTCGAGGCCCTCGGACCCCTGCTGAGCTCCCCACACGGCGTGGCC
GTGATGTCATGACCGTAGCCACTTCTGGCTGCGCTGCTGCCAGCTCTGCCAGTACCGCGTGTG
CCACAGGAACACGGCTTCTCTCGCTCTCTGAGGTGCTCTGCAGATGCTGAGTGGCTGCCAGCAGCCCTGG
GTGAGGG
GTGCGAGGG
CGTGGCGTACCGCACCCCTGAGGTCTGGGGAGCAGTGCAGCGTGGAGCCGGACCTGATCAGCAAAGTCTCCAG
GGGCTGATCGAGGTGAGGTCCCCCCCACCTGGAGGAGCTGCTGACTGCAATTCTCTGCTGCCACTGGGATGCTG
TCCCGGTTCCAGCTGTAAGGGCTTGTGGTGTGGAGCTCCCTGCTGCTGCCAGGGAGGAGCCCCCTGG
GGGAAGGGGGGTGCGGAGCTGGAGCTGCCAGGCTGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
CTGGAATGCTGGACCCCAGGGTGTCAAGCTGCCCCGACCTGCAAGCTGCTTCTCCGGAGGAAG
GCCAAAGTCAGGCCAGGG
ACACTGCAAGCTGATCGCATCCAGTCTGGGAGAAGCGGGGAAACAGGGTTGCAACCCCTCTGCTCTGGAC
TTCTCTGGGCTGATCATGTTCTGCCATCTGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
GAGCTGGTGTGCGGGTCAAGGGCCGGAGCTCATCAGCCTGGTGGAGCTGATCTGGCCAGGGGGAGACCGGG
AGCCAGGACGGGGGACACGCCGCTGCAAGCTCATCCGGGCTGGCCCTGCTGCTGAGCTGCTGTGG
GACGATGAGAGTGTCAAGGAAGGTGACGGGACACTCTGCAAGCTGCACTCCAGTGGGGAGACAGCGTGTGG
AGGGCTGCCAGAGACCTTCTCTGAGCTCTACAGCGGGGGGGAGCTCGGGGTGGGGTGCCTGAGGTCTTA
CTGCAAGCGAAGGGGCTGCCAGCAGCAGCGTCTGCAAGCTGGAGCGACTCATCCACCGCTTCACTACGCTCCTT
GCCGACACCGACAGACTCCGGGCTTGGAGAACCGGAGGGGGCGAGTGCCACATGGGCTGCCGAAGCTGGCG
GCCACCCGGCTGCTGCTGCAAGGACCTGCCATGATGCCGCTCTGCACGGCCGACCCACCTCAACTTC
CAGGAGTCCCGCAGCAGAACCCATGACTGCTTCTGCCACCTGCTGGGCTGCTGGAGCTGCTGCAACCG
GTGTTCCGAGCGAGCACAGGGGGCGCTGGGACTGCTTCTGCTCTCATCCGCTGCTGTAATTACAGG
AAAGCTCCCGCCCATCTGGCTCTGGCTCATCAAAAGTGTGAGCTCCATCCAAGTACATTACCTAACATGCC
CCAGCAGCCATCTCTTCTGCAAGAGCAGCCGACCCGCCCTCCACGACCTGCTTGCACAACAGTGACCTGG
ATGCTGAATACCTCTCTGAGGGCTCAGGCTGCCAGGACAGGAGGAGGAGGAGGAGGAGGAGGAG
GGCAGGGAGGAGAGCTAGCCGGCTCTTGGCCCTGGTCAAGCTGCTCTCTGTCACCCCTGACCGCGGCCAG
ATGCCCTACATAAAAGCGCTTCCCGGGGAAACGGTGGAGGATCTGAGTGGAGGTCTGAGTGACATAGAC
GAGATGTCCCGGGAGACCCGAGATCTCTGAGCTTCTCTGCCAGAACCTGAGCGGTGATGAGCTCGGGAG
GAGTGTGGCGCAACTCTGCCCTGAGCTGGCCCTGCCATGAGAACAGCCCGAGCATTCAGCGCTTTC
CTGCCAGCTCATGTAAGCTGCCAGGACTTGGAGGTGGTGCAGAGCGGCCCTCCGGAAACCTGCTGAG
TACGCTCTCTGCAAGAGCAGCCGGCTGCTGCTGCCACGGGCTTCTGGTGGGAGTGTACGCCAGATG
GACCCAGCGCGAGATCTCGAGGGGCTGAGGATCTGCAATGAGGGGGCTGATGTGAGCTGCG
CCCCCTCAAGCCCCGGCCGTCCGCTCCGGGGATCTCGAGGCAAAGCCAGGAACCGTGGCGITGGCTGG
TCTGTCAGGGAGGAGGTGAGGGGCCAGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
CTCCGGGGGGGGCTGGCATAGGGGCCCTGAGGCCAGCAAGCCCTCAATTCACTTCTGGGCCACAGCCCTGCCG
AGCGCGGAGATCCCCCGGGCATGGCCTGGGCTGGTTTGATGAAAGCAGCTGAACTGTCAA

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631
><subunit 1 of 1, 1029 aa, 1 stop
><MW: 114213, pI: 6.42, NX(S/T): 0

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IRSEVLRLVDAALQDLEPQQQLLFVQSFGIPVSSMSKLLQFLDQAVAHDPTLEQNIMDKNY
MAHLVEVQHHERGASGGQTFSLLTASLPPRRDSTEAPPKKSPEQPIGQGRIVVGTLRLVLG
PEDDLAGMFLOQIFPLSPDPRWQSSSPRPVALALQQALGQELARVQGSPEVPGITVRVLQAL
ATLLSPHPGGALVMSMRSHFLACPLLRQLCQYQRCPQDTGFSSLFLKVLLQMLQWLDSPG
VEGGPLRAQLRMLASQASAGRRLSDVRGGLLRLAEALAFRQDLEVVSVTRAVIATLRSGEQ
CSVEPDLSKVLQGLIEVRSPLHEELLTAFFSATADAASPFPACKPVVVVSSLLLQEEEPLA
GGKPGADGGSLEAVRLGPSSGLLWDLEMLDPREVSSCPDLQLRLLFSRRKGKGQAQVPSFR
PYLLTLFTHQSSWPTLHQCIRVLLGKSREQRFDPSASLDFLWACIHVPRIWQGRDQRTPQKR
REELVLRVQGPTELISLVELILAEAEATRSQDGDTAACSLIQARLPPLLSCCGDDESVRKVTE
HLSGCIQQWQGDSVLRGRCRDLLLQLYLQRPELRVPVPEVLLHSEGAASSSVCKLDGLIHRFI
TLLADTSDSRALENRGADASMACRKLAVAHPLLLRHLPMIAALLHGRTHLNQFQEFRQNHLS
SCFLHVLLGQHLLQHVFVRSEHQGALWDCLLSFIRLLLNYRKSSRHLAAFINKFVQFIHKYI
TYNAPAAISFLQKHADPLHDLSDFNSDLVMLKSSLAGLSLPSRDDRDTDRGLDEEGEEESSAG
SLPLVSVSLSFTPLTAAEMAPYMKRSLRGQTVEDLELVSDIDEMSRRPEILSFFSTNLQRL
MSSAAECCRNLAFSLRSMQNSPSIAAAFLPTFMYCLGSQDFEVVQTAJRNLPAYALLCQE
HAAVLLHRAFLVGMGYQMDPSAQISEALRILHMEAVM

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,
665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

FIGURE 17

CCGGGCCATGCAGCCTCGCCCCGCGGGCGCCCGCGCACCCGAGGAGATGAGGCTCCGC
AATGGCACCTTCTGTACGCTGCTCTTCCTGTGCGCTTCCCTCGCTGTCTGGTA
CGCGCACTCAGCGGCCAGAAAGGCAGCTGAGCAGGAGCCTCAAGCGCTCCAAGGGAGCTCAACCTG
TGCGCATCGGTTGACCGCAGCTGAGCAGGAGCCTCAAGCGCTCCAAGGGAGCTCAACCTG
GTGCTGGACGAGATCAAGAGGGCCGTGTCAGAAAGGCAGGCCGTGCGAGACGGAGACCGCAA
TCGCACCTGGGGCCGCTAACAGAGGACCCCATTGAAAGCGCTGGAAACGGCTCACACCGGC
ACGTGCTGCACCTGCCAACCGTCTCCATCACCTGCCAACACTGCTGGCCAAGGGAGAGCAGT
CTGAGCCTCGCGGTGGCGTGGGCCAGGGCCGACCGGAGTGTGGTGTGGTATGGGCATCCC
GAGCGTGCAGGCGCAGGGTGCACTCGTACCTGACTCGCAGCTCGCTCATCTCCGAGC
TGAGCCCGCAGGAGAAGGAGGACTCGGTATCGTGGTGTGATGCCGAGACTGACTCACAG
TACACTTGGCAGTGACAGAGAACATCAAGGCCCTTGTCCCCACGGAGATCCATTCTGGGCT
CCTGGAGGTATCTCACCCCTCCCCCACTTCTACCCCTGACTCTCCGCCCGAGAGTCCT
TTGGGGACCCCAAGGAGAGACTCAGGTGGAGGACCAAACAGAACCTCGATTACTGCTTCTC
ATGATGTCAGCGCAGTCCAAAGGCATCTACTACCGTGCAGCTGGAGGATGACATCGTGGCAA
GCCCAAACCTTGAGCACCATGAAGAACCTTGCAGTGACTCGCAGGCCCTCAGAGGAGCTGGATGA
TCCTGGAGTTCTCCAGCTGGCTTCAATTGGTAAGATGTTCAAGTGTGCTGGACCTGAGCCTG
ATTGTAGAGTTCAATTCTCATGTTTACCGGGACAAGGCCATCGACTGGCTCTGGACCATAT
TCTGTGGGTGAAAGTCTGCAACCCCGAGAAGGATGCGAAGCACTGTGACCGGAGAAAGCCA
ACCTCGGGATCCGCTTCAACCGTCCCTTCCAGCACGTGGGACTCACTCCTCGTGGCT
GGCAAGATCCAGAAACTGAAGGACAAAGACTTTGAAAGCAGGCGCTGCGAAGGAGCATGT
GAACCCCCAGCAGAGGTGAGCAGCAGGCCCTGAAGACATACCCAGCAGTACCTGGAGAAAG
CCTACCTGGCGAGGACTTCTCTGGGCTTCACCCCTGGCGGGGACTTCCATCCGCTT
CGCTTCTCCAACCTTCAAGACTGGAGCGGCTTCTCTCCGAGTGGAAACATCGAGCACCC
GGAGGACAAGCTTCAACACTGTGAGGAGGTGCTGCCCTTGACACAACCTCAGTCAGACA
AGGAGGCCCCCTGCAGGAGGGCGCACGCCACCCCTCCGGTACCTCGGAGCCCCGACGGCTAC
CTCCAGATCGGCTCTTCTACAAGGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTCGGCC
TCTGGAAAGCACTGCCCTCTGATCCAGACGGACTCCCTGTTGGGTGATTCTGAGCAGA
TCTTCTGAAAAAGGGCGACTTAAGCTGCCCTTCTGAGGGTACCCCTGTGGCCAGCCCTGAA
GCCCAACATTCTGGGGGTGTCGTACTGCCGTCCCGAGGGCCAGATAACGGCCCGCCCAA
AGGGTCTGCCCTGGCGTGGGCTTGGGCCCTGGGTCCGCCGTGGCCGGAGGCCCTA
GGAGCTGGTGTGCTGCCCGCCGGCGGGGGAGGGAGGAGGCCAGGGGGGGGGGGGGGGGG
TGAGGCCCCGGAACCGTTCGCACCCGGCTGCCCTGCCCCAGTCAGGGCTTTAGAAGAGCTTTAC
TTGGGCGCCGGCGCTCTGGCGAACACTGGAATGCTATACTACTTTATGTGCTGTGTT
TTTTTATTCTGGATACATTGATTTCACGTAAAGTCCACATATACTTCTATAAGAGCGTG
ACTTGTAATAAAGGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 18

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307
><subunit 1 of 1, 548 aa, 1 stop
><MW: 63198, pI: 8.10, NX(S/T): 4
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ELNLVLVDEIKRAVSERQALRGDGDNRTWGRLTEDPRLKPWNNGSHRHVLHLPTVFHHLPHLA
KESSLQPAPRVGQGRTGVSVVMGIPSVRREVHSYLTDTLHSLSISELSPQEKEHSVIVVLIAE
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLRESFGDPKERVRWRTKQNLD
YCFLMMYQAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL
DLSLIVEFILMFYRDKPIDWLDDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGTH
SSLAGKIQKLKDKGQALRKEHVNPRAEVSTSLKTYQHFTLEKAYLREDFFWAFTPAAGD
FIRFRFFQPLRLERFFFSGNIEHPEDKLFNTSVEVLPFDNPQSDKEALQEGRTATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAPFGPLEALRLSIQTDSPVVVILSEIFLKKAD
```

Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515